

## SUPPLEMENTAL MATERIAL

### SUPPLEMENTAL FIGURE LEGENDS

**Supplemental Figure 1. Pulmonary vacular leakage in LPS-treated WT and FAST<sup>-/-</sup> mice.** (A) The concentration of total protein in the BAL fluid from untreated and LPS-treated mice. Means  $\pm$  SEM are shown (n=7). Black bars represent WT mice and white bars represent FAST<sup>-/-</sup> mice. (B) Representative Diff-quick stained cytopins of LPS-recruited BAL cells (magnification: 63x). Arrow points to a neutrophil and arrowhead points to a red cell. \* $P < 0.05$ .

**Supplemental Figure 2. Quantification of FAST mRNA levels in neutrophils and lung.** Relative levels of FAST mRNA in lung and BM neutrophils from WT and FAST<sup>-/-</sup> mice, were measured by SYBR Green based real time quantitative PCR assay (see Materials and Methods for details).

**Supplemental Figure 3. Chemotaxis in FAST<sup>-/-</sup> neutrophils.** BM neutrophils isolated from WT and FAST<sup>-/-</sup> mice were exposed to 1  $\mu$ M fMLP in a chemotactic chamber EZ-TAXIScan and single motile cells were tracked for 20 minutes with frames taken every 30 seconds. Parameters of motility such as average migration speed, directionality and upward directionality are shown. Results are mean  $\pm$  SEM of n=20 cells for each group from 3 different movie sequences. Black bars represent WT mice and white bars represent FAST<sup>-/-</sup> mice. \* $P < 0.05$ .

**Supplemental Figure 4. ROS production by FAST<sup>-/-</sup> neutrophils.** WT and FAST<sup>-/-</sup> thioglycollate-elicited peritoneal neutrophils were activated with zymosan for the indicated times and ROS production was measured using luminol-dependent

chemiluminescence. RLU, relative light units. Black squares represent WT mice and white squares represent FAST<sup>-/-</sup> mice.

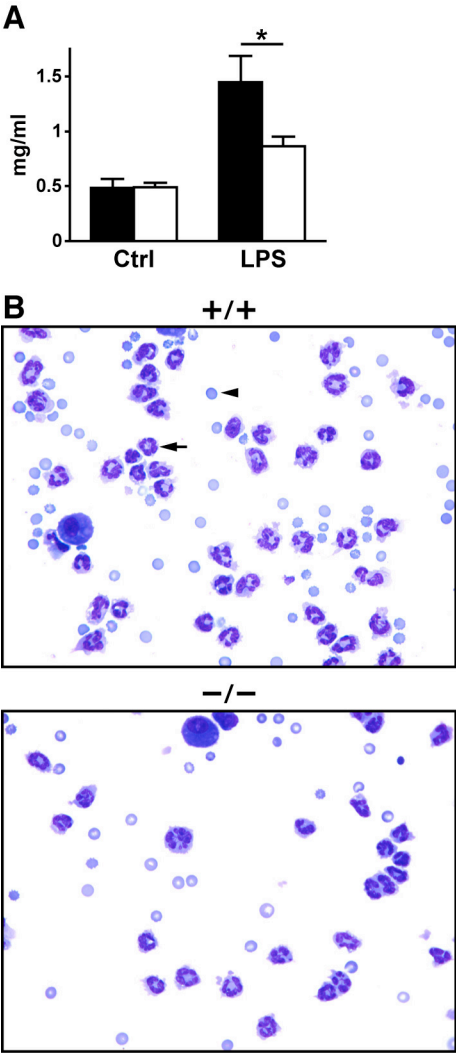
**Supplemental Figure 5. Analysis of engraftment efficiency in transplanted mice.**

PCR Analysis of engraftment efficiency using blood DNA from some of the transplanted mice in Figure 7. Primers MSG128 and MSG129 amplified a WT band (384 bp) and primers MSG105 and MSG133 amplified a KO band (669 bp). Primer sequences are provided in Supplemental Table I. Tail DNA was used for PCR genotyping of recipient mice. Numbers in this figure were used in the identification of the mice.

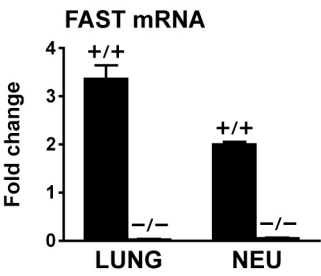
**Supplemental Figure 6. TNF- $\alpha$  levels in BAL fluid of LPS-treated chimeric mice.**

TNF- $\alpha$  levels were tested in the BAL fluid of mice in Figure 7. \* $P < 0.05$ ; \*\* $P < 0.01$ .

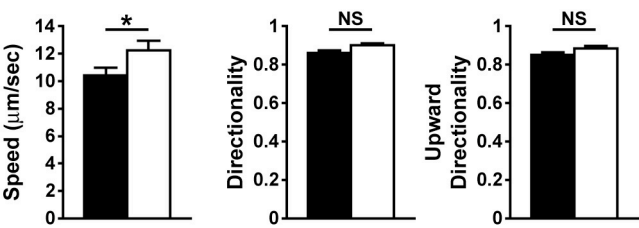
**Supplemental Figure 1**  
**Simarro, *et al.***



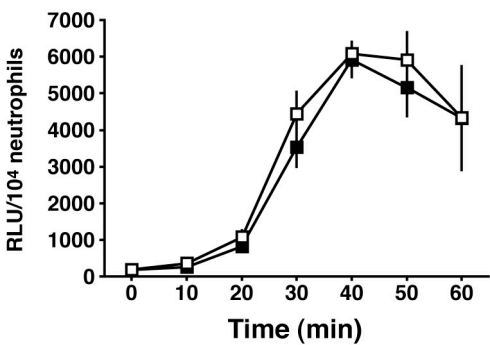
**Supplemental Figure 2**  
**Simarro, *et al.***



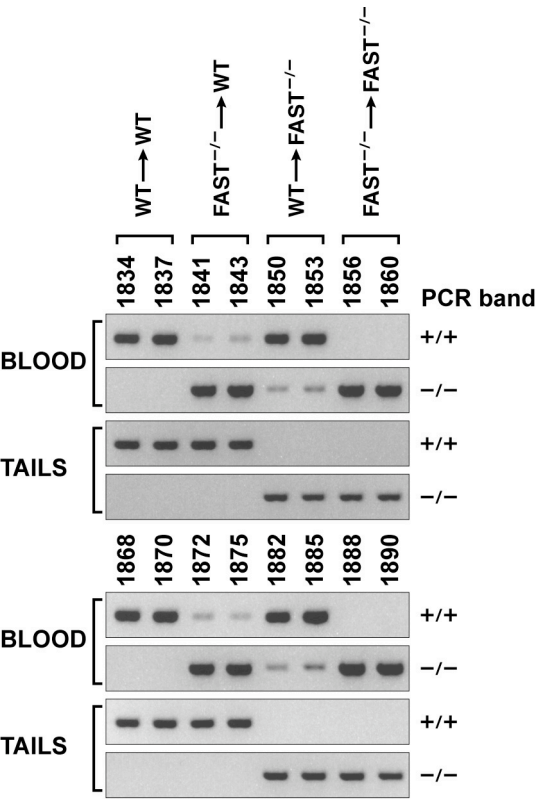
**Supplemental Figure 3**  
**Simarro, *et al.***



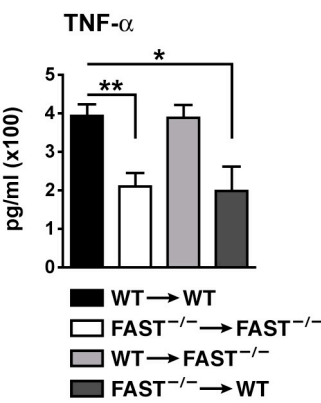
**Supplemental Figure 4**  
**Simarro, *et al.***



**Supplemental Figure 5**  
**Simarro, *et al.***



**Supplemental Figure 6**  
**Simarro, *et al.***



**Supplemental Table I**  
**Simarro, *et al.***

Primers used in this study.

	NAME	GENE	geneID	RefSeq		PRIMER SEQ
<b>MSG 76</b>	NOTI 5 ARM sense			NT_165760	genomic	TATAGCGGCGCGGCTATGTCACCATACCTTAGCC
<b>MSG 77</b>	SALI 5 ARM antisense			NT_165760	genomic	TATAGTCGACGCCGCCACCGAGTCGCGCATCTT
<b>MSG 105</b>	KO sense				cloning vector	CTCGAGGTCGACGGGTATCGATA
<b>MSG 128</b>	WT sense			NT_165760	genomic	GTGAATGACCTCAGGCTTAAC
<b>MSG 129</b>	WT antisense			NT_165760	genomic	AGAGAGCAGGATTCTGAAGCAT
<b>MSG 133</b>	KO antisense			NT_165760	genomic	AATCTTCACTGAGCGAGAAATG
<b>MSG 151</b>	GAPDH sense	GAPDH	14433	NM_008084	transcript	CATGACCAACAGTCCATGCCATCACT
<b>MSG 152</b>	GAPDH antisense	GAPDH	14433	NM_008084	transcript	TGAGGTCCACCAACCCCTGTTGCTGTA
<b>MSG 287</b>	b-actin sense	Actb	11461	NM_007393	transcript	GACATGGAGAAGATCTGGCA
<b>MSG 288</b>	b-actin antisense	Actb	11461	NM_007393	transcript	GGTCTCAACATGATCTGGGT
<b>MSG 299</b>	FAST sense	FASTK	66587	NM_023229	transcript	AGCTCAACAGCAAGGTGGTACAGA
<b>MSG 300</b>	FAST antisense	FASTK	66587	NM_023229	transcript	AAATGTTGACTGTGGCCAAGGGTG
<b>MSG 323</b>	HPRT1 sense	HPRT1	15452	NM_013556	transcript	GCGTCGTGATTAGCGATGATGAAC
<b>MSG 324</b>	HPRT1 antisense	HPRT1	15452	NM_013556	transcript	GAGCAAGTCTTTCAGTCCTGTCCA
<b>MSG 418</b>	P1			NT_165760	genomic	TCCTGAGTGCTCAAGCTACC
<b>MSG 419</b>	P2			NT_165760	genomic	GTGTAACCTGCTGTCTCCAGAGG